

Southern hybridizations were performed using enzymes that cleave in the DNA flanking the transgene insertion. Genomic DNA from plants of genotype GU-Ds-US, sAc and the uniform GUS+ plants were digested with EcoRV and hybridized with a probe specific for the 3' end of the GU-Ds-US construct (Figure 1). The probe hybridizes to the same 4.2 kb band in the GU-Ds-US progenitor plants and the uniform GUS+ plants. This result indicates that the two GUS+ plants could not have arisen by seed or pollen contamination, but did in fact originate by recombination of the GU-Ds-US transgene locus.

In the Claims

Please amend claims 1, 5-9, 18-20, 22-23, 25, 30, 33, and 35 as follows:

1. (Amended)

A method to induce homologous recombination in a plant, comprising introducing a recombination construct to the plant, and introducing a transposase to the plant, so as to induce homologous recombination.

5. (Amended)

A method to construct a functional gene in plants, comprising introducing to the plant a maize recombination construct having overlapping sequences having homologous regions, which sequences, when homologously recombined, result in a functional gene, and introducing a transposase to the plant, so as to induce recombination and construction of said functional gene.

6. (Amended)

The method of claim 5, wherein the functional gene is selected from the group consisting of: genes useful for disease resistance; genes useful for male sterility; genes useful for environmental condition tolerance; and genes useful for fruit ripening, oil or pigment biosynthesis, seed formation, and starch metabolism.

7. (Amended)

The method of claim 5, wherein the plant in which recombination is induced is selected from the group consisting of: soybean; maize; sugar cane; beet; tobacco; wheat; barley; poppy; rape; sunflower; alfalfa; sorghum; rose; carnation; gerbera; carrot; tomato; lettuce; chicory; pepper; melon; Arabidopsis; and cabbage.

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8. (Amended)

A method to induce recombination in a plant comprising introducing to the plant a maize Ds element containing overlapping sequences having homologous regions to a fragment of a gene; and introducing subsequently to the transformation of said Ds element a transposase, so as to induce homologous recombination and subsequent transcription of said gene.

9. (Amended)

The method of claim 8, wherein the gene is selected from the group consisting of: genes useful for disease resistance; genes useful for male sterility; genes useful for environmental condition tolerance; and genes useful for fruit ripening, oil or pigment biosynthesis, seed formation, and starch metabolism.

18. (Twice Amended)

A recombination construct which can be induced to undergo homologous recombination in the presence of a maize transposase, said construct comprising direct repeat sequences proximal to a Ds element and an agronomically significant gene internal to the direct repeats.

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19. (Amended)

A composition of matter which can be induced to undergo homologous recombination upon introduction of a maize transposase, said composition of matter comprising direct repeat sequences proximal to a Ds element and an agronomically significant gene internal to the direct repeats as part of a vector.

20. (Amended)

A composition of matter which can be induced to undergo homologous recombination upon introduction of a maize transposase comprising direct repeat sequences proximal to a Ds element and an agronomically significant gene internal to the direct repeats in a plant transformed with said construct.

22. (Amended)

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The composition of matter of claim 20, which further comprises a gene internal to said direct repeat sequences.

23. (Amended)

The composition of matter of claim 20, wherein said direct repeat sequences are in the form of overlapping sequences having homologous regions.

25. (Amended)

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The method of claim 24, wherein the agronomically significant gene is selected from the group consisting of: genes useful for disease resistance; genes useful for male sterility; genes useful for environmental condition tolerance; and genes useful for fruit ripening, oil or pigment biosynthesis, seed formation, and starch metabolism.

30. (Amended)

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The method of claim 2, wherein the maize Ds element is further defined as containing overlapping sequences having homologous regions, which sequences, when homologously combined, results in a functional gene.

33. (Amended)

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The method of claim 30, wherein the gene is selected from the group consisting of: genes useful for disease resistance; genes useful for male sterility; genes useful for environmental condition tolerance; and genes useful for fruit ripening, oil or pigment biosynthesis, seed formation, and starch metabolism.

35. (Amended)

The recombination construct of claim 18, wherein the gene is selected from the group consisting of: genes useful for disease resistance; genes useful for male sterility; genes useful for environmental condition tolerance; and genes useful fruit ripening, oil or pigment biosynthesis, seed formation, and starch metabolism.

3/12

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